

## IDENTIFICATION

**Species:** *Sphagnum fallax*

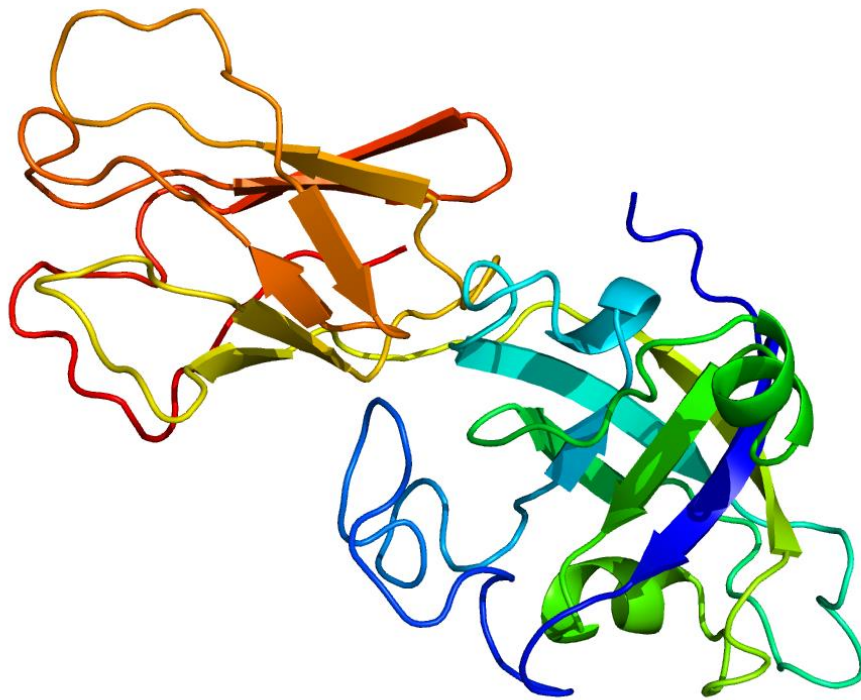
**Locus:** Sphfalx0047s0059

**Gene Model:** Sphfalx0047s0059.1.p

**Description:** SfEXPA-18

**Family:** Alpha Expansin

**3D structure:**



## GENOME DATABASES

Phytozome: [https://phytozome-next.jgi.doe.gov/info/Sfallax\\_v0\\_5](https://phytozome-next.jgi.doe.gov/info/Sfallax_v0_5)

KEGG:-

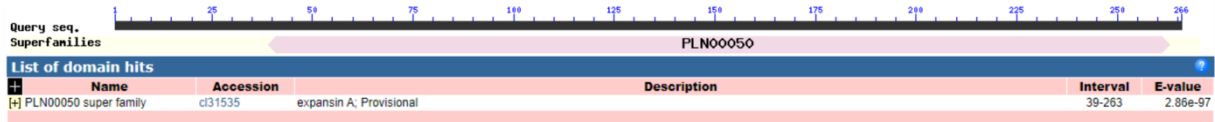
## EXTERNAL RESOURCES

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## GENE STRUCTURE



## DOMAIN ARCHITECTURE



## SEQUENCES

### Peptide

>SfEXPA-18

MATSTTSQYHFALVPQLLLLALAAALLFAGSVQCGGYTGTSWGSAHATFYGGADAS  
GTQGGACGYGNTYSTGYGVDTAALSSALFNSGLSCGACYQLICVDSWPCLGGNPGG  
ITVTATNFCPDGSNGGWCNPPLEHFDLAQPMFLQLAQERGGVVPVSYRRVACIKSGG  
MRFTINGNPFMLVLITNVGGAGDIQQVSVKGANTGSWYPLSRNWGQNWQYSGINL  
QSQPLSFSVTTSDGETVISNDVAPAYWQLGSTYEGAQFPE\*

### CDS (coding sequence)

>SfEXPA-18

ATGGCTACTTCCACCACCTCTCAGTACCATTTTGCCTAGTACCGCAACTCTTGCT  
GCTTGCACTTGCAGCCGCATTGCTTTTCGCGGGATCAGTTCAATGCGGAGGTTAC  
ACAGGAACTAGCTGGGGATCCGCACATGCAACTTTCTATGGTGGCGCTGATGCAT  
CCGGA ACTCAAGGTGGAGCTTGTGGGTATGGCAACACCTACAGCACAGGTTACG  
GAGTGGACACTGCGGCGCTCAGTTCGGCTCTCTTCAACAGTGGTCTCAGCTGTGG  
AGCTTGCTATCAGCTCATTGCGTGGATTCCCCTTGGTGCCTAGGAGGAAATCCTG  
GAGGGATTACAGTTACAGCCACAACTTCTGTCCCGACGGTTCTAATGGAGGCTG  
GTGTAACCCTCCTCTGGAACACTTTGATCTTGCGCAGCCCATGTTTTTGCAACTCG  
CACAGGAGCGGGGAGGAGTCGTACCTGTGAGCTACAGAAGAGTAGCCTGCATCA  
AATCTGGGGGAATGCGCTTACCATCAACGGAAACCCCTTCTTCATGCTGGTTCT  
CATCACCAACGTAGGAGGCGCAGGAGACATCCAGCAAGTGTCCGTCAAAGGAGC  
TAACACGGGAAGCTGGTACCCATTGAGCAGGAACTGGGGTCAAACTGGCAGTA  
CAGCGGCATTAACCTGCAGTCACAGCCACTGTCGTTTCAGCGTCACCACTAGCGAC  
GGCGAGACCGTGATTTCCAACGATGTAGCACCAGCGTACTGGCAACTGGGATCTA  
CATACGAGGGAGCACAATTCCCTGAATGA

### Nucleotide

>SfEXPA-18

GGTTGTTTCATCACTCAGCTACTGCCACTGCCTCTACGTGCCTGCCTGTCTTCATA  
ACTGAGACTCCGCGTTTTCTGTGCAGCAACTGCGCCAGCTGCAAGAAAGAATCTC  
CAGCCGTGTGCCAGCCAGTGCAACAACCCACAGCAGCAGCAGAAGAAGA  
AGAAGAAGTAGAGGAATTATGGCTACTTCCACCACCTCTCAGTACCATTTGCAC  
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GTGGATTTCCCTTGGTGCCTAGGAGGAAATCCTGGAGGGATTACAGTTACAGGTA  
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CAATCTCTTGAGCAAGCTTTTATATTCATGCCTACATTGGACTCTTCATCTGAGCA  
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CCGACGGTTCTAATGGAGGCTGGTGTAAACCCTCCTCTGGAACACTTTGATCTTGC  
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CAGCTCCACCCATGCTCGACCACCCATGCTGACTCCTGTAAACAGTATTTCTGACAC  
CCAAGATGAGTTCCTTACTTTTTTCGCAACCTCACCCATAAACTGAACTGGGATT  
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CATCAATCTAAATGCATAATATTCATGTTGA